

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2004, 05:03:03 ; Search time 1026 Seconds

(without alignments)  
7337.044 Million cell updates/sec

Title: US-10-009-570-1

Perfect score: 1772

Sequence: 1 acttagataataaagtaag.....ctcttccttcagtgcaag 1772

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

N\_Geneseq\_29Jan04:\*  
1: Geneseqn1980s:\*  
2: Geneseqn1990s:\*  
3: Geneseqn2000s:\*  
4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002s:\*  
7: Geneseqn2003as:\*  
8: Geneseqn2003bs:\*  
9: Geneseqn2003cs:\*  
10: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1772	100.0	1772	4	Aaf24785 Nucleotid
2	1772	100.0	1803	4	Aaf24787 Nucleotid
3	1772	100.0	2688	4	Aaf24791 Complete
4	1686	95.1	1686	4	Aaf24790 Nucleotid
5	660	37.2	2000	7	Ada73179 Rice gene
6	86	4.9	86	4	Aaf24788 Nucleotid
7	45	2.5	2000	7	Ada72764 Rice gene
8	34	1.9	2000	7	Ada72806 Rice gene
9	32	1.8	2000	7	Ada72521 Rice gene
10	30	1.7	2000	7	Ada73205 Rice gene
11	28	1.6	2000	7	Ada73342 Rice gene
12	28	1.6	5579	6	AAL46958 Rice lesi
13	26	1.5	2000	7	Ada73166 Rice gene
14	26	1.5	2000	7	Ada73198 Rice gene
15	24	1.4	676	4	Aaf81474 Corn prom
16	24	1.4	2000	7	Ada71850 Rice gene
17	24	1.4	2199	9	ADC08382 Rice DNA
18	23	1.3	1999	9	ADC08516 Rice DNA
19	23	1.3	2000	7	Ada71502 Rice gene
20	23	1.3	2000	7	Ada72983 Rice gene
21	23	1.3	2000	9	ADC08500 Rice DNA
22	23	1.3	5579	6	AAL46958 Rice lesi
23	23	1.3	6533	6	ABK28384 DNA trans

24	23	1.3	6544	4	AAS45340	Aas45340	Chemical
25	23	1.3	6544	6	ABL32646	ABL32646	Human imm
26	23	1.3	7442	4	AAS46686	Aas46686	Tumour su
27	23	1.3	9052	6	ABL32145	ABL32145	Human imm
28	23	1.3	9267	6	ABL33853	ABL33853	Human imm
29	23	1.3	9817	6	ABL33368	ABL33368	Human imm
30	23	1.3	90541	6	ABS52847	ABS52847	Human SR
31	23	1.3	113033	7	AAL54213	Aal54213	SR protei
32	22	1.2	22	4	Aaf24794	Aaf24794	PCR prime
33	22	1.2	1999	9	ADC08514	Adc08514	Rice DNA
34	22	1.2	2000	7	Ada72153	Ada72153	Rice gene
35	22	1.2	2000	7	Ada72089	Ada72089	Rice gene
36	22	1.2	2000	7	Ada73195	Ada73195	Rice gene
37	22	1.2	2000	7	Ada73343	Ada73343	Rice gene
38	22	1.2	2000	7	Ada73432	Ada73432	Rice gene
39	22	1.2	2000	7	Ada71502	Ada71502	Rice gene
40	22	1.2	2000	7	Ada73460	Ada73460	Rice gene
41	22	1.2	2000	7	Ada71850	Ada71850	Rice gene
42	22	1.2	2000	7	Ada72700	Ada72700	Rice gene
43	22	1.2	6061	6	ABL70591	ABl70591	Chemical
44	22	1.2	6061	6	AAS61302	Aas61302	Human gen
45	22	1.2	6185	6	ABL32412	ABL32412	Human imm

## ALIGNMENTS

### RESULT 1

AAF24785 ID AAF24785 standard; DNA; 1772 BP.  
XX AC AAF24785;  
XX AC AAF24785;  
DT 20-APR-2001 (first entry)  
XX DE Nucleotide sequence of a rice sucrose synthase 3 (RSus3) promoter.  
XX KW Rice; sucrose synthase 3 promoter; RSus3 promoter; endosperm expression;  
XX KW transgenic plant; carbohydrate metabolism; sucrose metabolism; ss.  
XX OS Oryza sativa.  
XX PN WO200078975-A2.  
XX PD 28-DEC-2000.  
XX PF 15-JUN-2000; 2000WO-GB002641.  
XX PR 17-JUN-1999; 99GB-00014210.  
XX PA (DANI-) DANISCO AS.  
XX PI Donaldson IA, Rasmussen TB;  
XX DR WPI; 2001-071398/08.  
XX PT Rice sucrose synthase 3 promoter obtainable from plant genus Oryza,  
XX PT useful for expressing nucleotide sequence of interest in specific tissue  
XX PS or cell type e.g. endosperm.  
XX CC Claim 1; Page 142; 144pp; English.  
XX CC The present sequence represents a rice sucrose synthase 3 (RSus3)  
XX CC promoter. The RSus3 promoter has low homology with the RSus1 and RSus2  
XX CC promoters (7.7% and 4.6%, respectively). In addition, apart from  
XX CC conserved TATA box and intron splice sites, they have no motifs in  
XX CC common. The promoter can be used to prepare a product of interest,  
XX CC especially in the endosperm of a transgenic plant. Preferably, the  
XX CC promoter is used to cause expression of a nucleotide of interest that can  
XX CC affect carbohydrate metabolism, such as sucrose metabolism, in a plant  
XX CC tissue  
XX SQ Sequence 1772 BP; 540 A; 368 C; 374 G; 490 T; 0 U; 0 Other;













```
XX
SQ Sequence 2000 BP; 623 A; 475 C; 360 G; 539 T; 0 U; 3 Other;

Query Match      2.5%; Score 45; DB 7; Length 2000;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 CAAATTTTAAAGACGAGTGGTCAACAGTACAGTAAAGAA 90
   |||||
DB 294 CAAATTTTAAAGACGAGTGGTCAACAGTACAGTAAAGAA 250

RESULT 8
ADA72806
ID ADA72806 standard; DNA; 2000 BP.
XX
AC ADA72806;
XX
DT 20-NOV-2003 (first entry)
XX
DE Rice gene, SEQ ID 6131.
XX
KW Plant; bacterial infection; fungal infection; viral infection; rice;
   gene; ds.
XX
OS Oryza sativa.
XX
PN WO2003000898-A1.
XX
PD 03-JAN-2003.
XX
PF 22-JUN-2001; 2001WO-IB001105.
XX
PR 22-JUN-2001; 2001WO-IB001105.
XX
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
XX
XX WPI; 2003-175290/17.
XX
PT Identifying at least one gene involved in plant resistance or response to
   pathogenic infection for conferring resistance or tolerance to a plant to
   bacterial, fungal or viral infection by determining or detecting plant
   gene expression.
XX
PS Claim 27; SEQ ID NO 6131; 899pp; English.
XX
CC The present invention relates to a method (M1) for identifying genes
   involved in plant resistance or response to pathogenic infection. M1
   comprises identifying a gene whose expression is significantly altered in
   the incompatible interaction of plant gene expression relative to
   the expression of the gene in an uninfected plant, in a mutant plant that
   does not express a gene associated with response to pathogenic infection,
   or in a corresponding incompatible or compatible interaction. (M1) is
   useful for conferring resistance to resistance or tolerance to a plant to
   bacterial, fungal or viral infection. The present sequence was used to
   illustrate the invention.
XX
SQ Sequence 2000 BP; 575 A; 481 C; 470 G; 467 T; 0 U; 7 Other;

Query Match      1.9%; Score 34; DB 7; Length 2000;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 TTTTAAATGAACGAGTGGTCAACAGTACAG 84
   |||||
DB 661 TTTTAAATGAACGAGTGGTCAACAGTACAG 694

RESULT 9
ADA72521
ID ADA72521 standard; DNA; 2000 BP.
XX
AC ADA72521;
XX
DT 20-NOV-2003 (first entry)
XX
DE Rice gene, SEQ ID 5846.
XX
KW Plant; bacterial infection; fungal infection; viral infection; rice;
   gene; ds.
XX
OS Oryza sativa.
XX
PN WO2003000898-A1.
XX
PD 03-JAN-2003.
XX
PF 22-JUN-2001; 2001WO-IB001105.
XX
PR 22-JUN-2001; 2001WO-IB001105.
XX
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
XX
XX WPI; 2003-175290/17.
XX
PT Identifying at least one gene involved in plant resistance or response to
   pathogenic infection for conferring resistance or tolerance to a plant to
   bacterial, fungal or viral infection by determining or detecting plant
   gene expression.
XX
PS Claim 27; SEQ ID NO 5846; 899pp; English.
XX
CC The present invention relates to a method (M1) for identifying genes
   involved in plant resistance or response to pathogenic infection. M1
   comprises identifying a gene whose expression is significantly altered in
   the incompatible interaction of plant gene expression relative to
   the expression of the gene in an uninfected plant, in a mutant plant that
   does not express a gene associated with response to pathogenic infection,
   or in a corresponding incompatible or compatible interaction. (M1) is
   useful for conferring resistance to resistance or tolerance to a plant to
   bacterial, fungal or viral infection. The present sequence was used to
   illustrate the invention.
XX
SQ Sequence 2000 BP; 649 A; 378 C; 372 G; 601 T; 0 U; 0 Other;

Query Match      1.8%; Score 32; DB 7; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 AAAATAAATAATAATCCAAATTTTAAATA 60
   |||||
DB 516 AAAATAAATAATAATCCAAATTTTAAATA 547

RESULT 10
ADA73205/c
ID ADA73205 standard; DNA; 2000 BP.
XX
AC ADA73205;
XX
DT 20-NOV-2003 (first entry)
XX
DE Rice gene, SEQ ID 6531.
XX
KW Plant; bacterial infection; fungal infection; viral infection; rice;
   gene; ds.
XX
OS Oryza sativa.
XX
PN WO2003000898-A1.
```



XX 03-JAN-2003.  
XX 22-JUN-2001; 2001WO-IB001105.  
XX 22-JUN-2001; 2001WO-IB001105.  
XX (SYGN ) SYNGENTA PARTICIPATIONS AG.  
XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;  
XX Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;  
XX WPI; 2003-175290/17.  
XX Identifying at least one gene involved in plant resistance or response to  
XX pathogenic infection for conferring resistance or tolerance to a plant to  
XX bacterial, fungal or viral infection by determining or detecting plant  
XX gene expression.  
XX Claim 27; SEQ ID NO 6531; 899pp; English.  
XX The present invention relates to a method (M1) for identifying genes  
XX involved in plant resistance or response to pathogenic infection. M1  
XX comprises identifying a gene whose expression is significantly altered in  
XX the incompatible interaction of plant gene expression relative to  
XX expression of the gene in an uninfected plant, in a mutant plant that  
XX does not express a gene associated with response to pathogenic infection,  
XX or in a corresponding incompatible or compatible interaction. (M1) is  
XX useful for conferring resistance to resistance or tolerance to a plant to  
XX bacterial, fungal or viral infection. The present sequence was used to  
XX illustrate the invention.  
XX Sequence 2000 BP; 613 A; 404 C; 328 G; 655 T; 0 U; 0 Other;  
XX  
XX Query Match 1.7%; Score 30; DB 7; Length 2000;  
XX Best Local Similarity 100.0%; Pred. NO. 0.0013;  
XX Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX QY 47 AAATTTTTTAAATAGACGAGTGGTCAAC 76  
XX |||||||  
XX Db 367 AAATTTTTTAAATAGACGAGTGGTCAAC 338  
XX |||||||  
XX  
XX RESULT 11  
XX ADA73342  
XX ID ADA73342 standard; DNA; 2000 BP.  
XX AC ADA73342;  
XX XX  
XX 20-NOV-2003 (first entry)  
XX DE Rice gene, SEQ ID 6668.  
XX XX  
XX Plant; bacterial infection; fungal infection; viral infection; rice;  
XX gene; ds.  
XX Oryza sativa.  
XX OS  
XX WO2003000898-A1.  
XX PN  
XX 03-JAN-2003.  
XX PD  
XX 22-JUN-2001; 2001WO-IB001105.  
XX PF  
XX 22-JUN-2001; 2001WO-IB001105.  
XX PR  
XX (SYGN ) SYNGENTA PARTICIPATIONS AG.  
XX PA  
XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;  
XX Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;  
XX WPI; 2003-175290/17.  
XX DR  
XX

PT Identifying at least one gene involved in plant resistance or response to  
PT pathogenic infection for conferring resistance or tolerance to a plant to  
PT bacterial, fungal or viral infection by determining or detecting plant  
PT gene expression.  
XX Claim 27; SEQ ID NO 6668; 899pp; English.  
XX The present invention relates to a method (M1) for identifying genes  
XX involved in plant resistance or response to pathogenic infection. M1  
XX comprises identifying a gene whose expression is significantly altered in  
XX the incompatible interaction of plant gene expression relative to  
XX expression of the gene in an uninfected plant, in a mutant plant that  
XX does not express a gene associated with response to pathogenic infection,  
XX or in a corresponding incompatible or compatible interaction. (M1) is  
XX useful for conferring resistance to resistance or tolerance to a plant to  
XX bacterial, fungal or viral infection. The present sequence was used to  
XX illustrate the invention.  
XX Sequence 2000 BP; 638 A; 344 C; 433 G; 583 T; 0 U; 2 Other;  
XX  
XX Query Match 1.6%; Score 28; DB 7; Length 2000;  
XX Best Local Similarity 100.0%; Pred. NO. 0.011;  
XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX QY 29 AAAATAAATAATAATCCAAATTTTTT 56  
XX |||||||  
XX Db 292 AAAATAAATAATAATCCAAATTTTTT 319  
XX |||||||  
XX  
XX RESULT 12  
XX AAL46958/c  
XX ID AAL46958 standard; cDNA; 5579 BP.  
XX XX  
XX AC AAL46958;  
XX XX  
XX 30-AUG-2002 (first entry)  
XX XX  
XX DE Rice lesion inhibitor protein Sp17 coding sequence.  
XX XX  
XX KW Rice; lesion formation inhibition; heat stress; agriculture; Sp17;  
XX KW transgenic; plant; horticulture; gene; ss.  
XX XX  
XX Oryza sativa.  
XX OS  
XX Key Location/Qualifiers  
XX exon 3177..3947  
XX FT /\*tag= b  
XX FT /number= 1  
XX FT CDS 3711..5327  
XX FT /\*tag= a  
XX FT /product= "Sp17"  
XX FT 3948..4184  
XX FT /\*tag= c  
XX FT /number= 1  
XX FT exon 4185..5327  
XX FT /\*tag= d  
XX FT /number= 2  
XX XX  
XX WO200233092-A1.  
XX PN  
XX 25-APR-2002.  
XX PD  
XX 18-OCT-2001; 2001WO-JP009153.  
XX PF  
XX 18-OCT-2000; 2000JP-00318557.  
XX PR  
XX (NAAG-) NAT INST AGROBIOLOGICAL SCI.  
XX PA  
XX Yano M, Yamanouchi U;  
XX PI  
XX WPI; 2002-372312/40.  
XX DR  
XX P-PSDB; AA017798.  
XX XX

PT Rice-originated gene, Spi17, that inhibits lesion formation and is  
PT applicable in improving heat stress of plants thus leading to prevention  
PT of lesion formation, for developing new breeds of plants for agriculture  
PT and horticulture.  
XX  
PS Claim 1; Page 30-40; 53pp; Japanese.  
XX  
CC The present invention provides the protein and coding sequences of rice  
CC lesion formation inhibitor Spi17. The protein improves the heat stress of  
CC the plant, and can be used in the development of new breeds of plants for  
CC agriculture and horticulture. The present sequence is the coding sequence  
CC of the invention  
XX  
SQ Sequence 5579 BP; 1453 A; 1272 C; 1235 G; 1619 T; 0 U; 0 Other;  
  
Query Match 1.6%; Score 28; DB 6; Length 5579;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 57 AATAAGACGAGTGGTCAACAGTACAG 84  
DB 2210 AATAAGACGAGTGGTCAACAGTACAG 2183  
|||||  
  
RESULT 13  
ADA73166/C  
ID ADA73166 standard; DNA; 2000 BP.  
XX  
AC ADA73166;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Rice gene, SEQ ID 6492.  
XX  
KW Plant; bacterial infection; fungal infection; viral infection; rice;  
KW gene; ds.  
XX  
OS Oryza sativa.  
XX  
PN WO2003000898-A1.  
XX  
PD 03-JAN-2003.  
XX  
PF 22-JUN-2001; 2001WO-IB001105.  
XX  
PR 22-JUN-2001; 2001WO-IB001105.  
XX  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
XX  
PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;  
PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;  
XX  
DR WPI; 2003-175290/17.  
XX  
PT Identifying at least one gene involved in plant resistance or response to  
PT pathogenic infection for conferring resistance or tolerance to a plant to  
PT bacterial, fungal or viral infection by determining or detecting plant  
PT gene expression.  
XX  
PS Claim 27; SEQ ID NO 6492; 899pp; English.  
XX  
CC The present invention relates to a method (M1) for identifying genes  
CC involved in plant resistance or response to pathogenic infection. M1  
CC comprises identifying a gene whose expression is significantly altered in  
CC the incompatible interaction of plant gene expression relative to  
CC expression of the gene in an uninfected plant, in a mutant plant that  
CC does not express a gene associated with response to pathogenic infection,  
CC or in a corresponding incompatible or compatible interaction. (M1) is  
CC useful for conferring resistance to resistance or tolerance to a plant to  
CC bacterial, fungal or viral infection. The present sequence was used to  
CC illustrate the invention.  
XX  
SQ Sequence 2000 BP; 492 A; 534 C; 468 G; 504 T; 0 U; 2 Other;  
  
Query Match 1.6%; Score 28; DB 6; Length 5579;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 57 AATAAGACGAGTGGTCAACAGTACAG 84  
DB 2210 AATAAGACGAGTGGTCAACAGTACAG 2183  
|||||  
  
RESULT 13  
ADA73166/C  
ID ADA73166 standard; DNA; 2000 BP.  
XX  
AC ADA73166;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Rice gene, SEQ ID 6492.  
XX  
KW Plant; bacterial infection; fungal infection; viral infection; rice;  
KW gene; ds.  
XX  
OS Oryza sativa.  
XX  
PN WO2003000898-A1.  
XX  
PD 03-JAN-2003.  
XX  
PF 22-JUN-2001; 2001WO-IB001105.  
XX  
PR 22-JUN-2001; 2001WO-IB001105.  
XX  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
XX  
PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;  
PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;  
XX  
DR WPI; 2003-175290/17.  
XX  
PT Identifying at least one gene involved in plant resistance or response to  
PT pathogenic infection for conferring resistance or tolerance to a plant to  
PT bacterial, fungal or viral infection by determining or detecting plant  
PT gene expression.  
XX  
PS Claim 27; SEQ ID NO 6492; 899pp; English.  
XX  
CC The present invention relates to a method (M1) for identifying genes  
CC involved in plant resistance or response to pathogenic infection. M1  
CC comprises identifying a gene whose expression is significantly altered in  
CC the incompatible interaction of plant gene expression relative to  
CC expression of the gene in an uninfected plant, in a mutant plant that  
CC does not express a gene associated with response to pathogenic infection,  
CC or in a corresponding incompatible or compatible interaction. (M1) is  
CC useful for conferring resistance to resistance or tolerance to a plant to  
CC bacterial, fungal or viral infection. The present sequence was used to  
CC illustrate the invention.  
XX  
SQ Sequence 2000 BP; 492 A; 534 C; 468 G; 504 T; 0 U; 2 Other;

Query Match 1.5%; Score 26; DB 7; Length 2000;  
Best Local Similarity 100.0%; Pred. No. 0.1;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 ACTTTAGATATAAAGTAAGTCACAA 26  
DB 1060 ACTTTAGATATAAAGTAAGTCACAA 1035  
|||||  
  
RESULT 14  
ADA73198  
ID ADA73198 standard; DNA; 2000 BP.  
XX  
AC ADA73198;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Rice gene, SEQ ID 6524.  
XX  
KW Plant; bacterial infection; fungal infection; viral infection; rice;  
KW gene; ds.  
XX  
OS Oryza sativa.  
XX  
PN WO2003000898-A1.  
XX  
PD 03-JAN-2003.  
XX  
PF 22-JUN-2001; 2001WO-IB001105.  
XX  
PR 22-JUN-2001; 2001WO-IB001105.  
XX  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
XX  
PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;  
PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;  
XX  
DR WPI; 2003-175290/17.  
XX  
PT Identifying at least one gene involved in plant resistance or response to  
PT pathogenic infection for conferring resistance or tolerance to a plant to  
PT bacterial, fungal or viral infection by determining or detecting plant  
PT gene expression.  
XX  
PS Claim 27; SEQ ID NO 6524; 899pp; English.  
XX  
CC The present invention relates to a method (M1) for identifying genes  
CC involved in plant resistance or response to pathogenic infection. M1  
CC comprises identifying a gene whose expression is significantly altered in  
CC the incompatible interaction of plant gene expression relative to  
CC expression of the gene in an uninfected plant, in a mutant plant that  
CC does not express a gene associated with response to pathogenic infection,  
CC or in a corresponding incompatible or compatible interaction. (M1) is  
CC useful for conferring resistance to resistance or tolerance to a plant to  
CC bacterial, fungal or viral infection. The present sequence was used to  
CC illustrate the invention.  
XX  
SQ Sequence 2000 BP; 633 A; 407 C; 355 G; 604 T; 0 U; 1 Other;  
  
Query Match 1.5%; Score 26; DB 7; Length 2000;  
Best Local Similarity 100.0%; Pred. No. 0.1;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 ACTTTAGATATAAAGTAAGTCACAA 26  
DB 108 ACTTTAGATATAAAGTAAGTCACAA 133  
|||||  
  
RESULT 15  
AAF81474/C  
ID AAF81474 standard; DNA; 676 BP.  
XX

AC AAF81474;  
XX  
DT 08-JUN-2001 (first entry)  
XX  
DE Corn promoter clone #700345819.  
XX  
KW Corn; promoter; transgenic plant; herbicide resistance; ds.  
XX  
OS Zea mays.  
XX  
FN WO200119976-A2.  
XX  
PD 22-MAR-2001.  
XX  
PF 13-SEP-2000; 2000WO-US025078.  
XX  
PR 16-SEP-1999; 99US-0154182P.  
XX  
PA (MONS ) MONSANTO CO.  
XX  
PI Anderson HM, Chay CA, Chen G, Conner TW;  
XX  
DR WPI; 2001-244796/25.  
XX  
PT Novel promoter nucleic acid sequences useful for regulating heterologous  
PT gene expression in plants, comprising regulatory sequences located  
PT upstream to plant DNA structural coding sequences.  
XX  
PS Claim 1; Page 98; 101pp; English.  
XX  
CC The present invention relates to novel corn promoter sequences (see  
CC AAF81456-AAF81478). The promoter sequences are useful for conferring  
CC expression of a second polynucleotide molecule in a transgenic plant  
CC tissue. In addition, the promoter sequences are useful for providing  
CC plants with herbicide resistance. The promoter sequences are suitable for  
CC selectively modulating expression of any operatively linked gene and  
CC provide additional regulatory element diversity in a plant expression  
CC vector in gene stacking approaches. The present sequence is one such corn  
CC promoter sequence isolated in the present invention  
XX  
SQ Sequence 676 BP; 210 A; 152 C; 119 G; 195 T; 0 U; 0 Other;

Query Match 1.4%; Score 24; DB 4; Length 676;  
Best Local Similarity 100.0%; Pred. No. 0.91;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 TTTTAAATAAGACGAGTGTCAA 74  
|||||  
Db 226 TTTTAAATAAGACGAGTGTCAA 203  
|||||

Search completed: October 2, 2004, 10:13:35  
Job time : 1029 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2004, 08:40:19 ; Search time 153 Seconds  
(without alignments)  
6427.274 Million cell updates/sec

Title: US-10-009-570-1  
Perfect score: 1772  
Sequence: 1 actctagataataagtaag.....ctcttctccttcagtcaag 1772

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA:\*

1: /cgn2\_6/ptodata/2/ina/5A COMB.seq.\*  
2: /cgn2\_6/ptodata/2/ina/5B COMB.seq.\*  
3: /cgn2\_6/ptodata/2/ina/6A COMB.seq.\*  
4: /cgn2\_6/ptodata/2/ina/6B COMB.seq.\*  
5: /cgn2\_6/ptodata/2/ina/PCTUS COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	24	1.4	676	US-09-665-189A-71	Sequence 71, Appl
C 2	23	1.3	90541	US-09-759-359A-3	Sequence 3, Appli
C 3	23	1.3	193303	US-09-497-855A-37	Sequence 37, Appl
C 4	23	1.3	193303	US-09-497-855A-44	Sequence 44, Appl
C 5	20	1.1	177	US-09-313-294A-292	Sequence 292, App
C 6	20	1.1	888	US-09-134-001C-13	Sequence 13, Appl
C 7	20	1.1	1462	US-08-464-517-30	Sequence 30, Appl
C 8	20	1.1	1462	US-08-246-361A-30	Sequence 30, Appl
C 9	20	1.1	1462	US-08-463-772-30	Sequence 30, Appl
C 10	20	1.1	1462	PCT-US93-05000-30	Sequence 30, Appl
C 11	19	1.1	531	US-08-642-274D-39	Sequence 39, Appl
C 12	19	1.1	531	US-08-352-014C-39	Sequence 39, Appl
C 13	19	1.1	573	US-09-134-001C-301	Sequence 301, App
C 14	19	1.1	851	US-09-495-050A-138	Sequence 138, App
C 15	19	1.1	2095	US-09-227-357-31	Sequence 31, Appl
C 16	19	1.1	6113	US-10-204-708-14	Sequence 14, Appl
C 17	19	1.1	6574	US-09-321-017B-1097	Sequence 1097, Ap
C 18	19	1.1	6669	US-10-204-708-6	Sequence 6, Appli
C 19	19	1.1	6678	US-08-816-617A-1	Sequence 1, Appli
C 20	19	1.1	11049	US-10-204-708-23	Sequence 23, Appl
C 21	19	1.1	25464	US-09-326-480A-4	Sequence 4, Appli
C 22	19	1.1	70000	US-09-851-896-3	Sequence 3, Appli
C 23	19	1.1	392000	US-10-027-983-11	Sequence 11, Appl
C 24	19	1.1	1830121	US-09-557-884-1	Sequence 1, Appli
C 25	19	1.1	1830121	US-09-643-990A-1	Sequence 1, Appli
C 26	18	1.0	405	US-09-621-976-15602	Sequence 15602, A
C 27	18	1.0	562	PCT-US92-03993-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-09-665-189A-71/c  
; Sequence 71, Application US/09665189A  
; Patent No. 6645765

GENERAL INFORMATION:

; APPLICANT: Anderson, Heather  
; APPLICANT: Chay, Catherine  
; APPLICANT: Chen, Guilan  
; APPLICANT: Conner, Timothy  
; TITLE OF INVENTION: Plant Regulatory Sequences for Control of Gene Expression  
; FILE REFERENCE: 38-211(15674)B  
; CURRENT APPLICATION NUMBER: US/09/665,189A  
; PRIOR FILING DATE: 2000-09-15  
; PRIOR APPLICATION NUMBER: 09/665,189  
; PRIOR FILING DATE: 2000-09-15  
; NUMBER OF SEQ ID NOS: 75  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 71  
; LENGTH: 676  
; TYPE: DNA  
; ORGANISM: Zea mays  
US-09-665-189A-71

Query Match 1.4%; Score 24; DB 4; Length 676;  
Best Local Similarity 100.0%; Pred. No. 0.13;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 TTTTAAATAAGACGAGTGTCAA 74  
|||||  
DB 226 TTTTAAATAAGACGAGTGTCAA 203

RESULT 2

US-09-759-359A-3/c  
; Sequence 3, Application US/09759359A  
; Patent No. 6492153

GENERAL INFORMATION:

; APPLICANT: ABU-THREIDEH, Jane et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; FILE REFERENCE: CL001043  
; CURRENT APPLICATION NUMBER: US/09/759,359A  
; CURRENT FILING DATE: 2001-01-16  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 90541  
; TYPE: DNA  
; ORGANISM: Human

## US-09-759-359A-3

Query Match 1.3%; Score 23; DB 4; Length 90541;  
Best Local Similarity 100.0%; Pred. No. 0.33;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 AAGTAAGTCACAGAAAATAAA 36  
DB 17920 AAGTAAGTCACAGAAAATAAA 17898

## RESULT 3

US-09-497-855A-37  
; Sequence 37, Application US/09497855A  
; Patent No. 6605432  
; GENERAL INFORMATION:  
; APPLICANT: Huang, Tim  
; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION  
; FILE REFERENCE: UMO1523  
; CURRENT APPLICATION NUMBER: US/09/497,855A  
; CURRENT FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: 60/120,592  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: 60/118,760  
; PRIOR FILING DATE: 1999-02-05  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 37  
; LENGTH: 193303  
; TYPE: DNA  
; ORGANISM: Homo sapiens;  
US-09-497-855A-37

Query Match 1.3%; Score 23; DB 4; Length 193303;  
Best Local Similarity 100.0%; Pred. No. 0.32;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1744 AGTTTCCTCCTCTCTCTCTCTCAG 1766  
DB 166834 AGTTTCCTCCTCTCTCTCTCTCAG 166856

## RESULT 4

US-09-497-855A-44  
; Sequence 44, Application US/09497855A  
; Patent No. 6605432  
; GENERAL INFORMATION:  
; APPLICANT: Huang, Tim  
; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION  
; FILE REFERENCE: UMO1523  
; CURRENT APPLICATION NUMBER: US/09/497,855A  
; CURRENT FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: 60/120,592  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: 60/118,760  
; PRIOR FILING DATE: 1999-02-05  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 44  
; LENGTH: 193303  
; TYPE: DNA  
; ORGANISM: Homo sapiens;  
US-09-497-855A-44

Query Match 1.3%; Score 23; DB 4; Length 193303;  
Best Local Similarity 100.0%; Pred. No. 0.32;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1744 AGTTTCCTCCTCTCTCTCTCTCAG 1766  
DB 166834 AGTTTCCTCCTCTCTCTCTCTCAG 166856

## RESULT 5

US-09-313-294A-292/c  
; Sequence 292, Application US/09313294A  
; Patent No. 6476212  
; GENERAL INFORMATION:  
; APPLICANT: Lalgudi, Raghunath V.  
; APPLICANT: Ito, Laura Y.  
; APPLICANT: Sherman, Bradley K.  
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR  
; FILE REFERENCE: PL-0017 US  
; CURRENT APPLICATION NUMBER: US/09/313,294A  
; CURRENT FILING DATE: 1999-05-14  
; NUMBER OF SEQ ID NOS: 7600  
; SOFTWARE: PERL Program  
; SEQ ID NO 292  
; LENGTH: 177  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. 6476212 700548929H1  
; NAME/KEY: unsure  
; LOCATION: 2, 6, 75-93  
; OTHER INFORMATION: a, t, c, g, or other  
US-09-313-294A-292

Query Match 1.1%; Score 20; DB 4; Length 177;  
Best Local Similarity 100.0%; Pred. No. 10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 950 AGCAGCAGCATGCATGCATG 969  
DB 59 AGCAGCAGCATGCATGCATG 40

## RESULT 6

US-09-134-001C-13/c  
; Sequence 13, Application US/09134001C  
; Patent No. 6380370  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134,001C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 13  
; LENGTH: 888  
; TYPE: DNA  
; ORGANISM: Staphylococcus epidermidis  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (505)  
; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.  
US-09-134-001C-13

Query Match 1.1%; Score 20; DB 4; Length 888;  
Best Local Similarity 100.0%; Pred. No. 9.9;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1285 GTTGTAACCCAGCAAAAT 1304  
DB 350 GTTGTAACCCAGCAAAAT 331

## RESULT 7

US-08-464-517-30  
; Sequence 30, Application US/08464517

```
; Patent No. 5869640
; GENERAL INFORMATION:
; APPLICANT: BEACH, David H.
; TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,517
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/963,308
; FILING DATE: 16-OCT-1992
; APPLICATION NUMBER: US 07/888,178
; FILING DATE: 26-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/701,514
; FILING DATE: 16-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Matthew P. Vincent
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MII-004C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1462 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(378..569, 662..1000, 1040..1189,
; LOCATION: 1191..1292, 1292..1324)
; US-08-464-517-30
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Query Match 1.1%; Score 20; DB 2; Length 1462;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 158 AAAAACAACAAACACAC 177
Db 310 AAAAACAACAAACACAC 329
```

```
RESULT 8
US-08-246-361A-30
; Sequence 30, Application US/08246361A
; Patent No. 5995582
; GENERAL INFORMATION:
; APPLICANT: BEACH, David H.
; TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
```

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/246,361A
; FILING DATE: 19-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/963,308
; FILING DATE: 16-OCT-1992
; APPLICATION NUMBER: US 07/888,178
; FILING DATE: 26-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/701,514
; FILING DATE: 16-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Matthew P. Vincent
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MII-004C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1462 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(378..569, 662..1000, 1040..1189,
; LOCATION: 1191..1292, 1292..1324)
; US-08-246-361A-30

Query Match 1.1%; Score 20; DB 2; Length 1462;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 158 AAAAACAACAAACACAC 177
Db 310 AAAAACAACAAACACAC 329

RESULT 9
US-08-463-772-30
; Sequence 30, Application US/08463772
; Patent No. 6066501
; GENERAL INFORMATION:
; APPLICANT: BEACH, David H.
; TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,772
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/963,308
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FILING DATE: 16-OCT-1992  
APPLICATION NUMBER: US 07/888,178  
FILING DATE: 26-MAY-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/701,514  
FILING DATE: 16-MAY-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Matthew P. Vincent  
REGISTRATION NUMBER: 36,709  
REFERENCE/DOCKET NUMBER: MII-004C  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1462 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: join(378..569, 662..1000, 1040..1189,  
LOCATION: 1191..1292, 1292..1324)  
US-08-463-772-30

Query Match 1.1%; Score 20; DB 3; Length 1462;  
Best Local Similarity 100.0%; Pred. No. 9.7; Indels 0; Gaps 0;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 158 AAAAACCAAAACACACAC 177  
Db 310 AAAAACCAAAACACACAC 329

RESULT 10  
US-08-952-014C-39  
Sequence 30, Application PC/TUS9305000  
GENERAL INFORMATION:  
APPLICANT: MITOXIX  
TITLE OF INVENTION: D-Type Cyclin and Uses Related Thereto  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: US  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/05000  
FILING DATE: 19930525  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/888,178  
FILING DATE: 26-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: CSHL91-02A  
TELEPHONE: 617-861-6240  
TELEFAX: 616-861-9540  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1462 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: double

TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
PCT-US93-05000-30  
Query Match 1.1%; Score 20; DB 5; Length 1462;  
Best Local Similarity 100.0%; Pred. No. 9.7; Indels 0; Gaps 0;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 158 AAAAACCAAAACACACAC 177  
Db 310 AAAAACCAAAACACACAC 329  
RESULT 11  
US-08-642-274D-39  
Sequence 39, Application US/08642274D  
PATENT NO. 6200749  
GENERAL INFORMATION:  
APPLICANT: Shiloh, Yosef  
TITLE OF INVENTION: MUTATED FORMS OF THE ATAXIA-TELANGIECTASIA GENE AND METHOD TO  
TITLE OF INVENTION: SCREEN FOR A PARTIAL A-T PHENOTYPE  
FILE REFERENCE: 22900033  
CURRENT APPLICATION NUMBER: US/08/642,274D  
CURRENT FILING DATE: 1996-05-03  
NUMBER OF SEQ ID NOS: 220  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 39  
LENGTH: 531  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: genomic  
US-08-642-274D-39

Query Match 1.1%; Score 19; DB 3; Length 531;  
Best Local Similarity 100.0%; Pred. No. 30; Indels 0; Gaps 0;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1321 AATTTAAATTTAGTTT 1339  
Db 105 AATTTAAATTTAGTTT 123

RESULT 12  
US-08-952-014C-39  
Sequence 39, Application US/08952014C  
PATENT NO. 6265158  
GENERAL INFORMATION:  
APPLICANT: Shiloh, Yosef  
TITLE OF INVENTION: ATAXIA-TELANGIECTASIA GENE AND ITS  
TITLE OF INVENTION: GENOMIC ORGANIZATION  
NUMBER OF SEQUENCES: 91  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kohn & Associates  
STREET: 30500 No. 6265158thwestern Hwy., Suite 410  
CITY: Farmington Hills  
STATE: Michigan  
COUNTRY: U.S.  
ZIP: 48334  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/952,014C  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Kohn, Kenneth I.  
REGISTRATION NUMBER: 30,995  
REFERENCE/DOCKET NUMBER: 2290.00028  
TELECOMMUNICATION INFORMATION:



```
;
; TELEPHONE: 810-539-5050
; TELEFAX: 810-539-5055
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 531 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-952-014C-39

Query Match
Best Local Similarity 1.1%; Score 19; DB 3; Length 531;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1321 AATTTAAATTTAGTTT 1339
Db 105 AATTTAAATTTAGTTT 123

RESULT 13
US-09-134-001C-301/c
; Sequence 301, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 301
; LENGTH: 573
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-301

Query Match
Best Local Similarity 1.1%; Score 19; DB 4; Length 573;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 710 TAAATCATTTTAGTTGCT 728
Db 99 TAAATCATTTTAGTTGCT 81

RESULT 14
US-09-495-050A-138/c
; Sequence 138, Application US/09495050A
; Patent No. 6492505
; GENERAL INFORMATION:
; APPLICANT: Roopa Reddy
; APPLICANT: Guegler, Karl, J.
; APPLICANT: Au-Young, Janice
; TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED P
; FILE REFERENCE: PA-0013 US
; CURRENT APPLICATION NUMBER: US/09/495,050A
; CURRENT FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/118,318
; PRIOR FILING DATE: February 1, 1999
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: PERL Program
; SEQ ID NO 138
; LENGTH: 851
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
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; OTHER INFORMATION: Incyte ID No. 6492505 1516908CB1
US-09-495-050A-138

Query Match
Best Local Similarity 1.1%; Score 19; DB 4; Length 851;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 AAAAAACAAACAAACA 174
Db 117 AAAAAACAAACAAACA 99

RESULT 15
US-09-227-357-31/c
; Sequence 31, Application US/09227357
; Patent No. 6342581
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: P2010P1
; CURRENT APPLICATION NUMBER: US/09/227,357
; CURRENT FILING DATE: 1999-01-08
; EARLIER APPLICATION NUMBER: PCT/US98/13684
; EARLIER FILING DATE: 1998-07-07
; EARLIER APPLICATION NUMBER: 60/051,926
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,793
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,925
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,929
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,803
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,732
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,931
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; EARLIER APPLICATION NUMBER: 60/051,916
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,930
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,918
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,920
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,733
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,795
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,919
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,928
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/055,722
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,723
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,948
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,949
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,953
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,950
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,947
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,964
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/056,360
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; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,684
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,984
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,954
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/058,785
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,664
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,660
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,661
; EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 31
; LENGTH: 2095
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (14)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-227-357-31

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Query Match      1.1%; Score 19; DB 4; Length 2095;
Best Local Similarity 100.0%; Pred.No. 28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 158 AAAAACCAAAACCAACACA 176
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Db 489 AAAAACCAAAACCAACACA 471

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Search completed: October 2, 2004, 15:15:58  
Job time : 157 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2004, 13:18:19 ; Search time 1196 Seconds

(without alignments)  
7511.097 Million cell updates/sec

Title: US-10-009-570-1

Perfect score: 1772

Sequence: 1 actttagataataagaag.....ctcttctcttcagtgaag 1772

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 3340653 seqs, 2534783454 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6681306

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA:\*

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- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*
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- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 14: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*
- 17: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 18: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 19: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	39	2.2	1610	17 US-10-437-963-7688	Sequence 7688, Ap
C 2	37	2.1	2981	17 US-10-437-963-92628	Sequence 92628, A
C 3	28	1.6	5579	13 US-10-168-2738-1	Sequence 1, Appli
C 4	27	1.5	2000	16 US-10-260-238-1731	Sequence 1731, Ap
C 5	26	1.5	630	17 US-10-437-963-27816	Sequence 27816, A
C 6	25	1.4	858	13 US-10-425-114-718	Sequence 718, App
C 7	25	1.4	2000	16 US-10-260-238-2163	Sequence 2163, Ap
C 8	25	1.4	6064	17 US-10-437-963-10006	Sequence 10006, A
C 9	25	1.4	3673778	15 US-10-312-841-2	Sequence 2, Appli
C 10	24	1.4	359	17 US-10-437-963-87728	Sequence 87728, A
C 11	24	1.4	390	13 US-10-424-593-64432	Sequence 64432, A
C 12	24	1.4	467	17 US-10-437-963-86792	Sequence 86792, A
C 13	24	1.4	1480	17 US-10-437-963-43365	Sequence 43365, A
C 14	24	1.4	2000	16 US-10-260-238-1731	Sequence 1731, Ap

C 15	23	1.3	433	17 US-10-437-963-4401	Sequence 4401, Ap
C 16	23	1.3	981	17 US-10-437-963-59741	Sequence 59741, A
C 17	23	1.3	1220	13 US-10-424-593-91213	Sequence 91213, A
C 18	23	1.3	1256	17 US-10-437-963-36681	Sequence 36681, A
C 19	23	1.3	2000	16 US-10-260-238-1664	Sequence 1, Appli
C 20	23	1.3	5579	13 US-10-168-2738-1	Sequence 1, Appli
C 21	23	1.3	6533	15 US-10-240-453-258	Sequence 258, App
C 22	23	1.3	6544	15 US-10-239-676-45	Sequence 45, Appli
C 23	23	1.3	6544	15 US-10-311-455-619	Sequence 619, App
C 24	23	1.3	7442	13 US-10-221-714A-409	Sequence 409, App
C 25	23	1.3	9052	15 US-10-311-455-118	Sequence 118, App
C 26	23	1.3	9267	15 US-10-311-455-1826	Sequence 1826, Ap
C 27	23	1.3	9817	15 US-10-311-455-1341	Sequence 1341, Ap
C 28	23	1.3	90541	9 US-09-759-359A-3	Sequence 3, Appli
C 29	23	1.3	90541	15 US-10-207-973-3	Sequence 3, Appli
C 30	23	1.3	90541	17 US-10-799-676-3	Sequence 3, Appli
C 31	23	1.3	193303	15 US-10-081-327-37	Sequence 37, Appli
C 32	23	1.3	193303	15 US-10-081-327-44	Sequence 44, Appli
C 33	23	1.3	3673778	15 US-10-312-841-1	Sequence 1, Appli
C 34	22	1.2	222	13 US-10-424-593-91097	Sequence 91097, A
C 35	22	1.2	574	13 US-10-425-114-12335	Sequence 12335, A
C 36	22	1.2	574	13 US-10-425-114-12359	Sequence 12359, A
C 37	22	1.2	1241	13 US-10-027-632-216612	Sequence 216612, A
C 38	22	1.2	1241	16 US-10-027-632-216612	Sequence 216612, A
C 39	22	1.2	1912	16 US-10-260-238-1722	Sequence 1722, Ap
C 40	22	1.2	2000	16 US-10-260-238-1963	Sequence 1963, Ap
C 41	22	1.2	2000	16 US-10-260-238-2448	Sequence 2448, Ap
C 42	22	1.2	3061	13 US-10-424-593-3866	Sequence 3866, Ap
C 43	22	1.2	6061	13 US-10-221-613-263	Sequence 263, App
C 44	22	1.2	6185	15 US-10-311-455-385	Sequence 385, App
C 45	22	1.2	7276	15 US-10-311-455-875	Sequence 875, App

## ALIGNMENTS

### RESULT 1

US-10-437-963-7688/c  
; Sequence 7688, Application US/10437963  
; Publication No. US2004012343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 7688  
; LENGTH: 1610  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_1425C.1  
US-10-437-963-7688

Query Match 2.2%; Score 39; DB 17; Length 1610;

Best Local Similarity 100.0%; Pred. No. 7.7e-09;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 815 CCAACGCTCACCAGTGGTGCCTCTCGACACGAGTTTA 853

Db 39 CCAACGCTCACCAGTGGTGCCTCTCGACACGAGTTTA 1

### RESULT 2

QY	57	AATAAGACGAGTGGTCAAAACAGTACAA	84
DB	2210	AATAAGACGAGTGGTCAAAACAGTACAA	2183

RESULT 4  
 US-10-260-238-1731/c  
 ; Sequence 1731, Application US/10260238  
 ; Publication No. US20040016025A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Budworth, Paul R.  
 ; APPLICANT: Moughamer, Todd G.  
 ; APPLICANT: Briggs, Steven P.  
 ; APPLICANT: Cooper, Bret  
 ; APPLICANT: Glazebrook, Jane  
 ; APPLICANT: Goff, Stephen A.  
 ; APPLICANT: Katagiri, Fumiya  
 ; APPLICANT: Kreps, Joel  
 ; APPLICANT: Provatt, Nicholas  
 ; APPLICANT: Ricke, Darrell  
 ; APPLICANT: Zhu, Tong  
 ; TITLE OF INVENTION: PROMOTERS FOR REGULATION  
 ; FILE REFERENCE: 60111-NP  
 ; CURRENT APPLICATION NUMBER: US/10/260,238  
 ; CURRENT FILING DATE: 2002-09-26  
 ; PRIOR APPLICATION NUMBER: US 60/325,448  
 ; PRIOR FILING DATE: 2001-09-26  
 ; PRIOR APPLICATION NUMBER: US 60/325,277  
 ; PRIOR FILING DATE: 2001-09-26  
 ; PRIOR APPLICATION NUMBER: US 60/370,620  
 ; PRIOR FILING DATE: 2002-04-04  
 ; NUMBER OF SEQ ID NOS: 6077  
 ; SEQ ID NO 1731  
 ; LENGTH: 2000  
 ; TYPE: DNA  
 ; ORGANISM: Oryza sativa  
 US-10-260-238-1731

Query Match 1.5%; Score 27; DB  
 Best Local Similarity 100.0%; Pred. No. 0.  
 Matches 27; Conservative 0; Mismatches

QY	57	AATAAGACGAGTGGTCAAAACAGTACAA	83
DB	1064	AATAAGACGAGTGGTCAAAACAGTACAA	1038

RESULT 5  
 US-10-437-963-27816  
 ; Sequence 27816, Application US/10437963  
 ; Publication No. US20040123343A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa, Thomas J.  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Cao, Yongwei  
 ; APPLICANT: Wu, Wei  
 ; APPLICANT: Boukharov, Andrey A.  
 ; APPLICANT: Barbaruk, Brad  
 ; APPLICANT: Li, Ping  
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecu  
 ; FILE REFERENCE: 38-21 (53221) B  
 ; CURRENT APPLICATION NUMBER: US/10/437,963  
 ; CURRENT FILING DATE: 2003-05-14  
 ; NUMBER OF SEQ ID NOS: 204966  
 ; SEQ ID NO 27816  
 ; LENGTH: 630  
 ; TYPE: DNA  
 ; ORGANISM: Oryza sativa  
 ; FEATURE:  
 ; NAME/KEY: unsure

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; LOCATION: (1)..(630)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_32474C.1
US-10-437-963-27816

Query Match      1.5%; Score 26; DB 17; Length 630;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTTTAGATAATAAGTAAGTCAAA 26
Db 428 ACTTTAGATAATAAGTAAGTCAAA 453

RESULT 6
US-10-425-114-718/c
; Sequence 718, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 718
; LENGTH: 858
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700087978_FLI
US-10-425-114-718

Query Match      1.4%; Score 25; DB 13; Length 858;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 ATTTTATTAATAGACGAGTGCTCA 73
Db 655 ATTTTATTAATAGACGAGTGCTCA 631

RESULT 7
US-10-260-238-2163
; Sequence 2163, Application US/10260238
; Publication No. US20040016025A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, Paul R.
; APPLICANT: Moughamer, Todd G.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiyaoki
; APPLICANT: Kreps, Joel
; APPLICANT: Provart, Nicholas
; APPLICANT: Ricke, Darrell
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
; FILE REFERENCE: 60111-NP
; CURRENT APPLICATION NUMBER: US/10/260,238
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/325,448
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
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; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 6077
; SEQ ID NO 2163
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-260-238-2163

Query Match      1.4%; Score 25; DB 16; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 AAAAAGCTCAAAATTCCTTATATAT 110
Db 81 AAAAAGCTCAAAATTCCTTATATAT 105

RESULT 8
US-10-437-963-10006/c
; Sequence 10006, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 10006
; LENGTH: 6064
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_16369C.1
US-10-437-963-10006

Query Match      1.4%; Score 25; DB 17; Length 6064;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 91 CTCAAAATTCCTTATATATATGGGAC 115
Db 3129 CTCAAAATTCCTTATATATATGGGAC 3105

RESULT 9
US-10-312-841-2
; Sequence 2, Application US/10312841
; Publication No. US20030186277A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MEC
; FILE REFERENCE: E01/1208/WO
; CURRENT APPLICATION NUMBER: US/10/312,841
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 3673778
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; FEATURE:
; NAME/KEY: unsure
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; LOCATION: (379615)  
US-10-312-841-2

Query Match 1.4%; Score 25; DB 15; Length 3673778;  
Best Local Similarity 100.0%; Pred. No. 0.2;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1322 ATTATTAATTTTACGTTTTTTTAA 1346  
Db 729897 ATTTAAATTTAGTTTTTTTTTA 729921

## RESULT 10

US-10-437-963-87728  
; Sequence 87728, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 87728  
; LENGTH: 359  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; LOCATION: (1)..(467)  
; OTHER INFORMATION: unsure at all n locations  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_86647C.1  
US-10-437-963-87728

Query Match 1.4%; Score 24; DB 17; Length 359;  
Best Local Similarity 100.0%; Pred. No. 0.33;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 GATATAAAGTAAGTCACAGAAA 30  
Db 309 GATATAAAGTAAGTCACAGAAA 332

## RESULT 11

US-10-424-599-64432  
; Sequence 64432, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 64432  
; LENGTH: 390  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_29194C.1  
US-10-424-599-64432

Query Match 1.4%; Score 24; DB 13; Length 390;  
Best Local Similarity 100.0%; Pred. No. 0.34;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 153 AAGAAAAAACAAAAACAAACACA 176  
Db 75 AAGAAAAAACAAAAACAAACACA 98

## RESULT 12

US-10-437-963-86792  
; Sequence 86792, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 86792  
; LENGTH: 467  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(467)  
; OTHER INFORMATION: unsure at all n locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_857C.1  
US-10-437-963-86792

Query Match 1.4%; Score 24; DB 17; Length 467;  
Best Local Similarity 100.0%; Pred. No. 0.34;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 116 TTATATTATGGACGGAGGAAGTA 139  
Db 373 TTATATTATGGACGGAGGAAGTA 396

## RESULT 13

US-10-437-963-43365/c  
; Sequence 43365, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 43365  
; LENGTH: 1480  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_46529C.1  
US-10-437-963-43365

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Query Match      1.4%; Score 24; DB 17; Length 1480;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTTAGATAATAAAGTAAGTCACAA 26
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Db 1285 TTTAGATAATAAAGTAAGTCACAA 1262

RESULT 14
US-10-260-238-1731
; Sequence 1731, Application US/10260238
; Publication No. US20040016025A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, Paul R.
; APPLICANT: Moughamer, Todd G.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiyaki
; APPLICANT: Kreps, Joel
; APPLICANT: Provart, Nicholas
; APPLICANT: Ricke, Darrell
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
; FILE REFERENCE: 60111-NP
; CURRENT APPLICATION NUMBER: US/10/260,238
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/325,448
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 6077
; SEQ ID NO 1731
; LENGTH: 2000
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; ORGANISM: Oryza sativa
US-10-260-238-1731

Query Match      1.4%; Score 24; DB 16; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 AATAAGACGAGTGGTCAACAGTA 80
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Db 1166 AATAAGACGAGTGGTCAACAGTA 1189

RESULT 15
US-10-437-963-4401/c
; Sequence 4401, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 4401
; LENGTH: 433
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; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_11289C.1
US-10-437-963-4401

Query Match      1.3%; Score 23; DB 17; Length 433;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 AATAAGACGAGTGGTCAACAGT 79
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Db 178 AATAAGACGAGTGGTCAACAGT 156

Search completed: October 2, 2004, 18:20:05
Job time : 1204 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 2, 2004, 05:05:33 ; Search time 11065 Seconds  
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Scoring table: OLIGO\_NUC  
Gapop 60.0, Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size: 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

GenEmbl:

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- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
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- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
- 15: em\_ba.\*
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- 18: em\_in.\*
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- 36: em\_htg\_man.\*
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- 38: em\_sy.\*
- 39: em\_htgo\_hum.\*
- 40: em\_htgo\_mus.\*
- 41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1772	100.0	1772	6	AX063520	Sequence
2	1772	100.0	1803	6	AX063522	Sequence
3	1686	95.1	1686	6	AX063525	Sequence
4	947	53.4	168173	8	AP004988	Oryza sat
5	660	37.2	2000	6	AX656635	Sequence
6	86	4.9	86	6	AX063523	Sequence
7	55	3.1	2771	8	AK100306	Oryza sat
8	52	2.9	139653	2	AP005890	Oryza sat
9	52	2.9	163555	2	AP005912	Oryza sat
10	50	2.8	135594	8	AC087220	Oryza sat
11	48	2.7	124366	8	AC131374	Oryza sat
12	48	2.7	150465	8	AC091749	Oryza sat
13	48	2.7	300029	8	AE017076	Oryza sat
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15	45	2.5	4817	8	AF254558	Oryza sat
16	45	2.5	139043	2	AC090974	Oryza sat
17	45	2.5	183580	8	AP003561	Oryza sat
18	44	2.5	137852	8	AP003880	Oryza sat
19	40	2.3	127506	8	OSJN00096	Sequence
20	40	2.3	167269	8	OSJN00085	Oryza sat
21	38	2.1	112483	2	AP004060	Oryza sat
22	38	2.1	132151	8	AC144491	Oryza sat
23	38	2.1	149807	2	AC120533	Oryza sat
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25	38	2.1	158291	8	AP004776	Oryza sat
26	38	2.1	159290	2	AP004813	Oryza sat
27	38	2.1	160562	2	AP005613	Oryza sat
28	38	2.1	168430	8	AC126221	Oryza sat
29	37	2.1	158815	8	AP003105	Oryza sat
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33	36	2.0	152058	8	AP005740	Oryza sat
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41	35	2.0	159626	8	AP005803	Oryza sat
42	35	2.0	173522	8	OSJN00060	Oryza sat
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ALIGNMENTS

RESULT 1  
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LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

AX063520  
Sequence 1 from Patent WO078975.  
AX063520  
AX063520.1 GI:12541259

synthetic construct  
synthetic construct  
artificial sequences.  
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Donaldson, I.A. and Rasmussen, T.B.  
Rice sucrose synthase promoter  
Patent: WO 0078975-A 1 28-DEC-2000;  
DANISCO A/S (DK)

1772 bp  
DNA  
linear  
PAT 24-JAN-2001







1  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Sasaki, T., Matsumoto, T. and Yamamoto, K.  
Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, BAC  
clone: B1056G08  
Published Only in Database (2002)  
2 (bases 1 to 168173)  
Sasaki, T., Matsumoto, T. and Yamamoto, K.  
Direct Submission  
Submitted (27-MAR-2002) Takuji Sasaki, National Institute of  
Agrobiological Sciences, Rice Genome Research Program, Kannondai  
2-1-2, Tsukuba, Ibaraki 305-8602, Japan  
(E-mail: tsasaki@ias.affrc.go.jp, URL: <http://rgp.dna.affrc.go.jp/>,  
Tel: 81-298-38-7441, Fax: 81-298-38-7468)  
On Oct 16, 2002 this sequence version replaced gi:22212589.  
Genes were predicted from the integrated results of the following:  
GENSCAN (<http://CCR-081.mit.edu/GENSCAN.html>), FGENESH  
(<http://www.softberry.com/>), GeneMark.hmm  
(<http://opal.biology.gatech.edu/GeneMark/>), GlimmerM  
([http://www.tigr.org/tdb/glimmer/glmr\\_form.html](http://www.tigr.org/tdb/glimmer/glmr_form.html)), RiceHMM  
(<http://rgp.dna.affrc.go.jp/RiceHMM/>), SplicePredictor  
(<http://bioinformatics.iastate.edu/cgi-bin/sp.cgi>), sim4  
(<http://globin.cse.psu.edu/hmli/docs/sim4.html>), gap2  
(<http://www.tigr.org/software/glimmer/>), BLASTN and BLASTX. The  
genomic sequence was searched against NCBI NonRedundant Protein  
database, nr (<ftp://ncbi.nlm.nih.gov/blast/db>) and the cDNA  
sequence database at RGP or DBJ. Protein homologies of the coding  
regions were searched against NCBI NonRedundant Protein database  
with BLASTP. ESTs represent the identified cDNA sequences using  
BLASTN with the corresponding DBJ accession no. and RGP clone ID.  
Full-length cDNAs represent the identified cDNA sequences using  
BLASTN with the corresponding DBJ accession no.  
A gene with identity or significant homology to a protein is  
classified based on the protein name to indicate the homology level  
such as same name, 'putative-' and '-like protein'. A gene without  
significant homology to any protein but with full-length cDNA or  
EST homology (covering almost the entire length of partial  
sequence) is classified as an 'unknown' protein. A gene predicted  
by two or more gene prediction programs is classified as a  
'hypothetical' protein according to IRGSP standard. A gene  
predicted by a single gene prediction program is also classified as  
a probable 'hypothetical' protein and is included as a  
miscellaneous feature of the sequence.  
The orientation of the sequence is from M13rev to -21M13 of the BAC  
clone. This is a partial sequence of B1056G08 clone. This sequence  
of B1056G08 clone has an overlap with P0616D06 (DBJ: AP005198) at  
5' end and an overlap with P0552F09 clone (DBJ: AP004309) at 3' end  
and an overlap with P056B08 clone (DBJ: AP004309) at 3' end.  
Detailed information on overlap and assembly quality together with  
annotation of this entry is available at  
<http://rgp.dna.affrc.go.jp/GenomeSeq.html>.

Location/Qualifiers  
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FEATURES  
source

gene

mRNA

CDS



Db 68884 GAACAGATATTAGTGCAACAGACAAATGCGCAACGCAATTTTTCTGTTTACCGGCAAGCT 68943  
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RESULT 5  
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LOCUS Sequence 6505 from Patent WO03000898. 2000 bp DNA linear PAT 22-MAR-2003  
DEFINITION  
ACCESSION AX656635  
VERSION AX656635.1 GI:29159449  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa  
Oryza sativa  
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE  
1 Chang, H.S., Chen, W., Cooper, B., Glazebrook, J., Goff, S.A., Hou, Y.M.,  
Katagiri, F., Qian, S., Tao, Y., Whitham, S., Xie, Z., Zhu, T. and Zou, G.  
Plant genes involved in defense against pathogens  
Patent: WO 03000898-A 6505 03-JAN-2003;  
Syngenta Participations AG (CH)  
Location/Qualifiers  
1. .2000  
/organism="Oryza sativa"  
/mol\_type="unassigned DNA"  
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Best Local Similarity 99.4%; Pred. No. 0;  
Matches 1090; Conservative 0; Mismatches 5; Indels 2; Gaps 1;  
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Db 61 TCCTTCATTTTCTACCACTATCAACCATAGCTCAACCGATCAATTCAGAAATAGTT 120  
Qy 789 ACTAAAGCATCGCTCATCACACACCAACCGCTCAGCGATGGTCTCTCGACACACGA 848  
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Db 241 TTTAGCGTTCGTTTCATGACGCTTCCACGCGACAGAGCTGAGCAGCAGATGATGCAT 300  
Qy 969 GGCTCTTGTGAAACAAAGGTTACTGGTAAATGACATGCTGCTAGCTAGTTAGCA 1028

Db 301 GGCTCTTGTGAAACAAAGGTTACTGTAATGACATGCTGCTGTAGCTAGTAGCA 360  
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Db 361 GAATGCAAGGCCCATGATATGCAATGCTATGCAACAAAGTATAGTACAGCATGTATGGT 420  
Qy 1089 AGCCAGTAACTAATCTATCAGCAGAGGCGAGAGCTCGTGCATGGTGTGATGCACTTCT 1148  
Db 421 AGCCAGTAACTAATCTATCAGCAGAGGCGAGAGCTCGTGCATGGTGTGATGCACTTCT 480  
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Db 601 GGTTCCTGTTAAACCGTTGGTAAACCCAGCAAAATAGACAAAATTTGTCAAAATTTTAA 660  
Qy 1329 ATTTTAG- -TTTTTTTTTAACTTAGCCGGGAAACCTTGAAGTTTGTGCTGTGAGCTGT 1386  
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Qy 1507 GCTTTTACGATCCCATACCGCGCTTGTGCAAAACCTGCCAAGAGAGCAGCAGAAACA 1566  
Db 841 GCTTTTACGATCCCATACAGCGCTTGTGCAAAACCTGCCAAGAGAGCAGCAGAAACA 900  
Qy 1567 GGTGTCAATTTTGGTGAAGAGCCAAAGTAAAGTAAACAGAAAGATGGAAGATAGTAGGAC 1626  
Db 901 GGTGTCAATTTTGGTGAAGAGCCAAAGTAAAGTAAACAGAAAGATGGAAGATAGTAGGAC 960  
Qy 1627 CAGGAGTGAAGGAGGAGACACATGGCCACGCTCCCTGCACATTTTCGTGTATAAATA 1686  
Db 961 CAGGAGTGAAGGAGGAGACACATGGCCACGCTCCCTGCACATTTTCGTGTATAAATA 1020  
Qy 1687 CAGTGGATGCATCGCTCTCCAGCATCCATCGTTCTCTGCTCTGTTTCATCCATAGT 1746  
Db 1021 CAGTGGATGCATCGCTCTCCAGCATCCATCGTTCTCTGCTCTGTTTCATCCATAGT 1080  
Qy 1747 TTCCTCTCTCTCTCTCT 1763  
Db 1081 TTCCTCTCTCTCTCTCT 1097

RESULT 6  
AX063523  
LOCUS Sequence 4 from Patent WO0078975. 86 bp DNA linear PAT 24-JAN-2001  
DEFINITION  
ACCESSION AX063523  
VERSION AX063523.1 GI:12541262  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
artificial construct  
artificial sequences.  
REFERENCE  
1 Donaldson, I.A. and Rasmussen, T.B.  
Rice sucrose synthase promoter  
Patent: WO 0078975-A 4 28-DEC-2000;  
DANISCO A/S (DK)  
Location/Qualifiers  
1. .86







**JOURNAL**  
**REFERENCE** 2 (bases 1 to 139653)  
**AUTHORS** Sasaki, T., Matsumoto, T. and Katayose, Y.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (13-NOV-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan  
 (E-mail: tsasakia@nias.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/, Tel: 81-298-38-7441, Fax: 81-298-38-7468)  
**COMMENT** NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.  
 \* NOTE: This is a 'working draft' sequence.  
 \* This sequence will be replaced  
 \* by the finished sequence as soon as it is available and  
 \* the accession number will be preserved.

**FEATURES**  
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 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="genomic DNA"  
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 Best Local Similarity 100.0%; Pred. No. 3.3e-16;  
 Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AAAAATAAATAATTCCTCAAAATTTTAAATAGACGAGTGTCAACAGT 79  
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**RESULT** 9  
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**DEFINITION** Oryza sativa (japonica cultivar-group) chromosome 9 clone OSJNBa0064123, \*\*\* SEQUENCING IN PROGRESS \*\*\*.  
**ACCESSION** AP005912  
**VERSION** AP005912.1  
**KEYWORDS** HTG; HTGS PHASE2  
**SOURCE** Oryza sativa (japonica cultivar-group)  
**ORGANISM** Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

**REFERENCE** 1  
**AUTHORS** Sasaki, T., Matsumoto, T. and Katayose, Y.  
**TITLE** Oryza sativa nipponbare (GA3) genomic DNA, chromosome 9, BAC clone: OSJNBa0064123  
**JOURNAL** Published Only in Database (2002)  
**REFERENCE** 2 (bases 1 to 163555)  
**AUTHORS** Sasaki, T., Matsumoto, T. and Katayose, Y.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (21-NOV-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan  
 (E-mail: tsasakia@nias.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/, Tel: 81-298-38-7441, Fax: 81-298-38-7468)  
**COMMENT** NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.  
 \* NOTE: This is a 'working draft' sequence.  
 \* This sequence will be replaced  
 \* by the finished sequence as soon as it is available and

**FEATURES**  
 source  
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 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="genomic DNA"  
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**ORIGIN**  
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 Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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**RESULT** 10  
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**DEFINITION** Oryza sativa chromosome 3 BAC OSJNB0097F01 genomic sequence, complete sequence.  
**ACCESSION** AC087220  
**VERSION** AC087220.9  
**KEYWORDS** HTG.  
**SOURCE** Oryza sativa (japonica cultivar-group)  
**ORGANISM** Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

**REFERENCE** 1 (bases 1 to 135594)  
**AUTHORS** Buell, C.R., Yuan, Q., Ouyang, S., Liu, J., Gansberger, K., Jones, K.M., Overton, I.L., Tsitrin, T., Kim, M.M., Bera, J.J., Jin, S.S., Fadrosch, D.W., Tallon, L.J., Koo, H., Zismann, V., Heiao, J., Blunt, S., Vanaken, S.S., Riedmuller, S.B., Utterback, T.T., Feldblum, T.V., Yang, Q.Q., Haas, B.J., Suh, B.B., Peterson, J.J., Quackenbush, J.J., White, O., Salzberg, S.L. and Fraser, C.M.  
**TITLE** Oryza sativa chromosome 3 BAC OSJNB0097F01 genomic sequence  
**JOURNAL** Unpublished  
**REFERENCE** 2 (bases 1 to 135594)  
**AUTHORS** Buell, R.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (15-DEC-2000) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA  
**REFERENCE** 3 (bases 1 to 135594)  
**AUTHORS** Buell, R.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (21-FEB-2003) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA  
**REFERENCE** 4 (bases 1 to 135594)  
**AUTHORS** Buell, R.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (12-MAR-2003) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA, rbuelletigr.org  
 On Feb 21, 2003 this sequence version replaced gi:16418178.  
**COMMENT** Address all correspondence to: rice@tigr.org

BAC clone OSJNB0097F01 is from Oryza sativa chromosome 3  
 The orientation of the sequence is from SP6 to T7 end of the BAC clone.  
 Genes were identified by a combination of several methods: Gene prediction programs including Fgenesh (<http://www.softberry.com/>), genscan and Genscan+ (Chris Burge, <http://CCR-081.mit.edu/GENSCAN.html>), GeneMarkHM (Mark Borodovsky, <http://genemark.biology.gatech.edu/GeneMark/>), and GeneSplicer (Mihaela Pertea and Steven Salzberg, [contact mperete@tigr.org](http://contact.mperete@tigr.org)), searches of the complete sequence against a peptide database and the plant EST database at TIGR (<http://www.tigr.org/tdb/tgi.shtml>). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named

after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy,  
http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats are identified by RepeatMasker (Arian Smit,  
http://ftp.genome.washington.edu/RM/RepeatMasker.html).

This BAC overlaps with rice BAC OSJNBa0013M12 (AC082644) and OSJNBa0090L05 (AC084765).

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## repeat\_region

## gene

## mRNA

## CDS

## repeat\_region

## repeat\_region

## repeat\_region

## repeat\_region

## repeat\_region

## repeat\_region

## repeat\_region

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Query Match      2.8%; Score 50; DB 8; Length 135594;
Best Local Similarity 100.0%; Pred. No. 4e-15;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GATAATAAGTCAACAGAAAAATAAATAAATCCAAATTTTTT 56
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Db 52161 GATAATAAGTCAACAGAAAAATAAATAAATCCAAATTTTTT 52112

RESULT 11
AC1131374      124366 bp      DNA      linear      PLN 03-SEP-2002
LOCUS
DEFINITION      Oryza sativa (japonica cultivar-group) chromosome 10 clone
OSJNB0008A05, complete sequence.
AC1131374
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 124366)
Wing,R.A., Yu,Y., Soderlund,C., Kim,H.-R., Rambo,T., Saski,C.,
Currie,J. and Collura,K.
Rice Genomic Sequence
Unpublished
2 (bases 1 to 124366)
Wing,R.A., Yu,Y., Soderlund,C., Kim,H.-R., Rambo,T., Saski,C.,
Currie,J. and Collura,K.
Direct Submission
TITLE
JOURNAL
REFERENCE
1 (bases 1 to 124366)
Wing,R.A., Yu,Y., Soderlund,C., Kim,H., Rambo,T., Saski,C.,
Currie,J., Collura,K. and Thurmond,S.K.
Direct Submission
TITLE
JOURNAL
REFERENCE
1 (bases 1 to 124366)
Wing,R.A., Yu,Y., Soderlund,C., Kim,H., Rambo,T., Saski,C.,
Currie,J., Collura,K. and Thurmond,S.K.
Direct Submission
COMMENT
The following sequence is an artificial clone that will be used for
gap filling in the rice genome. There is 100 kb of sequence from
the overlapping north clone (OSJNB0008A05) and 7982 bases of
sequence from the overlapping south clone (OSJNB0027A14) and the
gap filling sequence begins at 100,001 and ends at 116,384 for a
total size of 124,366 bases. The gap filling sequence is 16,384
bases. The name (OSJNB0008A05) was derived from the location of
the north clone and the 'A' stands for Artificial.
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Best Local Similarity 100.0%; Pred. No. 4.9e-14;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 30 AAATAAATAAATAATCCAAATTTTTTAAATAGACGAGTGGTCAACA 77
|||||
Db 68083 AAATAAATAAATAATCCAAATTTTTTAAATAGACGAGTGGTCAACA 68130
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AC091749 150465 bp DNA linear PLN 13-NOV-2001
Oryza sativa chromosome 10 BAC OSJNB0008A05 genomic sequence,
complete sequence.
AC091749
AC091749.8 GI:16445110
HTG.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 150465)
Buell, C.R., Yuan, Q., Ouyang, S., Liu, J., Moffat, K.S., Hill, J.N.,
Gansberger, K., Brenner, M., Burgess, S., Hance, M., Shvartsbeyn, M.,
Tsitrin, T., Riggs, F., Hsiao, J., Zismann, V., Blunt, S., Pai, G.,
VanAken, S.E., Utterback, T.R., Feldblyum, T.V., Kalb, E.,
Quackenbush, J., Salzberg, S.L., White, O. and Fraser, C.M.
Oryza sativa chromosome 10 BAC OSJNB0008A05 genomic sequence
Unpublished
2 (bases 1 to 150465)
Buell, R.
Direct Submission
Submitted (30-MAY-2001) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
3 (bases 1 to 150465)
Buell, R.
Direct Submission
Submitted (26-OCT-2001) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
4 (bases 1 to 150465)
Buell, R.
Direct Submission
Submitted (13-NOV-2001) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA, rbuell@tigr.org
On Oct 26, 2001 this sequence version replaced gi:15808580.
Address all correspondence to:rice@tigr.org

BAC clone OSJNB0008A05 is from Oryza sativa chromosome 10
The orientation of the sequence is from SP6 to T7 end of the BAC
clone.
Genes were identified by a combination of several methods: Gene
prediction programs including Fgenesh (http://www.softberry.com/),
genscan and Genscan+ (Chris Burge,
http://CCR-081.mit.edu/GENSCAN.html), GeneMarkHM (Mark Borodovsky,
http://genemark.biology.gatech.edu/Genemark/), and GeneSplicer
(Mihaela Pertea and Steven Salzberg, contact mpertea@tigr.org),
searches of the complete sequence against a peptide database and
the plant EST database at TIGR (http://www.tigr.org/tdb/tgi.shtml).
Annotated genes are named to indicate the level of evidence for
their annotation. Genes with similarity to other proteins are named
after the database hits. Genes without significant peptide
similarity but with EST similarity are named as unknown proteins.
Genes without protein or EST similarity, that are predicted by more
than two gene prediction programs over most of their length are
annotated as hypothetical proteins. Genes encoding tRNAs are
predicted by tRNAscan-SE (Sean Eddy,
http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats are
identified by RepeatMasker (Arian Smit,
http://ftp.genome.washington.edu/RM/RepeatMasker.html).
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This BAC overlaps with rice BAC OSJNBa0073L20.

location/Qualifiers  
1..150465

/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="genomic DNA"



AB017076	ORyza sativa	300029 bp	DNA	linear	PLN 06-JUN-2003	mrna
LOCUS	ORyza sativa (japonica cultivar-group)	300029 bp	DNA	linear	PLN 06-JUN-2003	
DEFINITION	ORyza sativa (japonica cultivar-group) chromosome 10, section 30 of 77 of the complete sequence.					
ACCESSION	AE017076	AE016959				CDS
VERSION	AE017076.1	GI:31431167				
KEYWORDS						
SOURCE	ORyza sativa (japonica cultivar-group)					
ORGANISM	ORyza sativa (japonica cultivar-group)					
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.					
AUTHORS	1 (bases 1 to 300029)					
CONSTRM						
TITLE	The Rice Chromosome 10 Sequencing Consortium					
JOURNAL	In-depth view of structure, activity, and evolution of rice chromosome 10					
REFERENCE	Science 300, 1566-1569 (2003)					
AUTHORS	Buell, C.R., Wang, R.A., McCombie, W.R., Messing, J. and Yuan, Q.					
TITLE	Direct Submission					
JOURNAL	Submitted (05-MAY-2003) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA					
COMMENT	This is the pseudomolecule for rice chromosome 10, which was constructed by resolving discrepancies between overlapping BACs, trimming the overlap regions, and linking the unique sequences to form a contiguous sequence. Genes in individual BAC clone were identified by a combination of several methods: Gene prediction programs, searches of the complete sequence against a peptide database and EST databases. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/).					
FEATURES	Location/Qualifiers					
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	/chromosome="10"					
misc_feature	<1..90733					
	/note="Chromosome Sequence Derivation: nucleotide sequence in this region was derived from BAC clone OSUNBa0093109 (GB:AC090486)."					
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gene						
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2004, 07:17:19 ; Search time 6888 Seconds  
(without alignments)  
7682.315 Million cell updates/sec

Title: US-10-009-570-1

Perfect score: 1772

Sequence: 1 actttagataataagaag.....ctcttctcttcagtgaag 1772

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*  
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3: em\_estin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_pbg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	50	2.8	628	28	AQ686477 nbxb0072B
2	38	2.1	748	28	AQ686991 nbxb0032J
C 3	30	1.7	569	28	AQ272200 nbxb0027L
4	30	1.7	629	14	CA754682 BR0300040

29	1.6	537	28	AQ510840	AQ510840 nbxb0094A
29	1.6	537	28	AQ510840	AQ510840 nbxb0094A
28	1.6	331	29	CG408907	CG408907 DS601.DS
28	1.6	409	28	AQ331226	AQ331226 nbxb0049E
28	1.6	452	28	AQ860090	AQ860090 nbxb0014I
28	1.6	466	28	AQ863506	AQ863506 nbxb0021O
28	1.6	623	28	AQ258100	AQ258100 nbxb0019P
28	1.6	652	12	BM420232	BM420232 U004F12.O
28	1.6	694	28	BZ692356	BZ692356 SP_Ba001
28	1.6	783	29	CC692659	CC692659 OGTA120TH
28	1.6	787	29	CC692657	CC692657 OGTA120TH
28	1.6	833	29	CG164014	CG164014 PUJAY17TD
28	1.6	856	28	AQ258985	AQ258985 nbxb0021P
28	1.6	887	29	CC704404	CC704404 OGOBQ28TH
27	1.5	525	28	BH776225	BH776225 f2mb013FO
27	1.5	728	14	CB663138	CB663138 OSJNB007M
27	1.5	898	28	AQ914858	AQ914858 nbxb0050I
26	1.5	162	29	AG025502	AG025502 Oryza sat
26	1.5	296	29	CC833513	CC833513 ZMMBB018
26	1.5	475	12	BI323424	BI323424 kt71B05.Y
26	1.5	493	12	BI450665	BI450665 kt73B08.Y
26	1.5	660	28	AQ287509	AQ287509 nbxb0030K
26	1.5	663	28	AQ872280	AQ872280 nbxb0047D
26	1.5	663	28	AQ872280	AQ872280 nbxb0047D
26	1.5	670	28	BZ786579	BZ786579 PUGDU05TD
26	1.5	677	28	CC400206	CC400206 PUEFS37TD
26	1.5	708	29	CG371013	CG371013 OGYAS24TH
26	1.5	712	29	CG916678	CG916678 ZMMBB038
26	1.5	761	28	AQ158754	AQ158754 nbxb0012G
26	1.5	798	28	AZ126642	AZ126642 OSJNB007
26	1.5	810	29	CC760816	CC760816 ZMMBB015
26	1.5	841	29	CG734891	CG734891 ZMMBB029
26	1.5	862	28	BZ962486	BZ962486 PUGDU05TB
26	1.5	898	28	AQ914858	AQ914858 nbxb0050I
26	1.5	970	28	CC370662	CC370662 PUEGK16TD
40	25	531	28	CC037205	CC037205 3591.1.85
41	25	566	28	BH788889	BH788889 f2mb021FO
42	25	566	28	CC019996	CC019996 3591.1.17
43	25	637	28	AQ510347	AQ510347 nbxb0095C
44	25	651	29	CG286906	CG286906 OGSAR02TC
25	1.4	678	29	CG007640	CG007640 ZUADY94TH

#### ALIGNMENTS

#### RESULT 1

AQ686477/c

#### LOCUS

#### DEFINITION

AQ686477 628 bp DNA linear GSS 01-JUL-1999  
nbxb0072B19r CUGI Rice BAC Library Oryza sativa (japonica  
cultivar-group) genomic clone nbxb0072B19r, genomic survey  
sequence.

#### ACCESSION

AQ686477

#### VERSION

AQ686477.1 GI:5327645

#### KEYWORDS

GSS.

#### SOURCE

Oryza sativa (japonica cultivar-group)

#### ORGANISM

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 628)

Wing, R.A. and Dean, R.A.

A BAC End Sequencing Framework to Sequence the Rice Genome

Unpublished (1998)

Contact: Wing RA

Clemson University

Clemson University Genomics Institute

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293

Email: rwing@clemson.edu

Seq primer: GGAAACAGCTATGACCATG

Class: BAC ends

High quality sequence stop: 384.

FEATURES  
source

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1..628
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
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/lab_host="E. coli DH10B"
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/note="Vector: pBeloBAC11; Site 1: HindIII; Site 2: HindIII; Rice is one of two most popular grains in the world. Half of the world population especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety. The library contains 36,864 clones with an average insert size of 128.5 Kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."
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ORIGIN

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Query Match 2.8%; Score 50; DB 28; Length 628;
Best Local Similarity 100.0%; Pred. No. 2e-09;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GATATAAGTAAGTCACAGAAAATAATAATTCCTCAATTTT 56
DB 485 GATATAAGTAAGTCACAGAAAATAATAATTCCTCAATTTT 436
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ORIGIN

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Query Match 2.8%; Score 50; DB 28; Length 628;
Best Local Similarity 100.0%; Pred. No. 2e-09;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 7 GATATAAGTAAGTCACAGAAAATAATAATTCCTCAATTTT 56
DB 485 GATATAAGTAAGTCACAGAAAATAATAATTCCTCAATTTT 436
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RESULT 2

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AQ868991 748 bp DNA linear GSS 03-NOV-1999
LOCUS nbxb0032J14r CUGI Rice BAC Library (EcoRI) Oryza sativa (japonica cultivar-group) genomic clone nbxb0032J14r, genomic survey sequence.
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ACCESSION AQ868991
VERSION AQ868991.1 GI:6219442
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SOURCE  
ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 748)

AUTHORS Wing, R.A. and Dean, R.A.  
TITLE A BAC End Sequencing Framework to Sequence the Rice Genome  
JOURNAL Unpublished (1998)  
COMMENT Contact: Wing RA

Clemson University  
Clemson University Genomics Institute

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293

Email: rwing@clemson.edu

Seq primer: GGAAACAGCTATGACCATG

Class: BAC ends

High quality sequence start: 34

High quality sequence stop: 416.

Location/Qualifiers

1..748

FEATURES

source

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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/strain="Japonica"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="nbxb0032J14r"
/tissue_type="Leaf"
/lab_host="E. coli DH10B"
/clone_lib="CUGI Rice BAC Library (EcoRI)"
/note="Vector: pBeloBAC11; Site 1: EcoRI; Site 2: EcoRI; Rice is the most important food crop in the world. Half of the world population, especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety using EcoRI as the cloning enzyme. The library contains 55,296 clones with an average insert size of 121 Kb providing approximately 15 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Three high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening and can be requested from the Clemson University BAC/EST Resource Center (www.genome.clemson.edu)."
```

ORIGIN

```
Query Match 2.1%; Score 38; DB 28; Length 748;
```

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Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 29 AAAATAATAATAATTCCTCAATTTTAAATAAGACGA 66
DB 425 AAAATAATAATAATTCCTCAATTTTAAATAAGACGA 462
```

RESULT 3

```
AQ272200/c
```

LOCUS

DEFINITION

nbxb0027L15f CUGI Rice BAC Library Oryza sativa (japonica cultivar-group) genomic clone nbxb0027L15f, genomic survey sequence.

ACCESSION AQ272200

VERSION AQ272200.1 GI:3825515

KEYWORDS GSS.

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 569)

AUTHORS Wing, R.A. and Dean, R.A.

TITLE A BAC End Sequencing Framework to Sequence the Rice Genome

JOURNAL Unpublished (1998)

COMMENT Contact: Wing RA

Clemson University

Clemson University Genomics Institute

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293

Email: rwing@clemson.edu

Seq primer: TAATACGACTCACTATAGG

Class: BAC ends

High quality sequence stop: 316.

Location/Qualifiers

1..569

FEATURES

source

```
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
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/strain="Japonica"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="nbxb0027L15f"
/tissue_type="Leaf"
/lab_host="E. coli DH10B"
/clone_lib="CUGI Rice BAC Library"
/note="Vector: pBelOBAC11; Site 1: HindIII; Site 2: HindIII; Rice is one of two most popular grains in the world. Half of the world population especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety. The library contains 36,864 clones with an average insert size of 128.5 Kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."

ORIGIN
Query Match      1.7%; Score 30; DB 28; Length 569;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 AAAATAAATAATATTCCTCAAAATTTTAA 58
    |||||||
Db 496 AAAATAAATAATATTCCTCAAAATTTTAA 467

RESULT 4
CA754682
LOCUS
DEFINITION
BR030004000_PLATE_E02_13_017.ab1 OA Oryza sativa (japonica cultivar-group) cDNA clone BR030004000_PLATE_E02_13_017.ab1 similar to No protein alignment, mRNA sequence.
ACCESSION
CA754682
VERSION
KEYWORDS
SOURCE
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 629)
Bohnert,H.J., Borchert,C., Brazille,S., Brooks,J., Eaton,M., Ferreira,H., Kawasaki,S., McCollough,A., Michalowski,C.B., Palacio,C., Scara,G., Wheeler,M. and Zepeda,G.R.
Functional Genomics of Plant Stress Tolerance
Unpublished (2000)
Contact: Mark Fredrickson
Department of Plant Biology
University of Illinois
1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 2172655473
Email: bohnertlab@life.uiuc.edu.
FEATURES
source
1..629
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="BR030004000_PLATE_E02_13_017.ab1"
/tissue_type="roots"
/dev_stage="3-4 weeks"
/clone_lib="OA"

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/note="19 h 200mM NaCl"

ORIGIN
Query Match      1.7%; Score 30; DB 14; Length 629;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 AAATTTTAAAGACGAGTGTGCTCAAC 76
    |||||||
Db 230 AAATTTTAAAGACGAGTGTGCTCAAC 259

RESULT 5
AQ510840
LOCUS
DEFINITION
nxb0094A05r CUGI Rice BAC Library Oryza sativa (japonica cultivar-group) genomic clone nxb0094A05r, genomic survey sequence.
ACCESSION
AQ510840
VERSION
AQ510840.1 GI:4732218
KEYWORDS
GSS.
SOURCE
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 537)
Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome
Unpublished (1998)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: twing@clemson.edu
Seq primer: GGAACAGCTATGACCATG
Class: BAC ends
High quality sequence start: 59
High quality sequence stop: 437.
FEATURES
source
1..537
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/cultivar="Japonica"
/strain="Nipponbare"
/db_xref="taxon:39947"
/clone="nxb0094A05r"
/tissue_type="Leaf"
/lab_host="E. coli DH10B"
/clone_lib="CUGI Rice BAC Library"
/note="Vector: pBelOBAC11; Site 1: HindIII; Site 2: HindIII; Rice is one of two most popular grains in the world. Half of the world population especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety. The library contains 36,864 clones with an average insert size of 128.5 Kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."

```

ORIGIN

Query Match 1.6%; Score 29; DB 28; Length 537;  
 Best Local Similarity 100.0%; Pred. No. 0.58;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 AATTTTATAAGACGAGTGGTCAAC 76  
 |||||  
 Db 508 AATTTTATAAGACGAGTGGTCAAC 536

RESULT 6  
 LOCUS AQ510840/c  
 DEFINITION nbx0094A05r CUGI Rice BAC Library Oryza sativa (japonica cultivar-group) genomic clone nbx0094A05r, genomic survey sequence.

ACCESSION AQ510840  
 VERSION AQ510840.1 GI:4732218  
 KEYWORDS GSS.  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 537)  
 AUTHORS Wing, R.A. and Dean, R.A.  
 TITLE A BAC End Sequencing Framework to Sequence the Rice Genome  
 JOURNAL Unpublished (1998)  
 COMMENT Contact: Wing RA

Clemson University Genomics Institute  
 Clemson University  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Tel: 864 656 7288  
 Fax: 864 656 4293

Email: rwing@clemson.edu  
 Seq primer: GGAAACAGCTATGACATG  
 Class: BAC ends  
 High quality sequence start: 59  
 High quality sequence stop: 437.

FEATURES  
 source  
 Location/Qualifiers

1..537  
 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="genomic DNA"  
 /strain="Japonica"  
 /cultivar="Nipponbare"  
 /db\_xref="taxon:39947"  
 /clone="nbx0094A05r"  
 /tissue\_type="Leaf"  
 /lab\_host="E. coli DH10B"  
 /clone\_lib="CUGI Rice BAC Library"  
 /note="Vector: pBelobAC11; Site 1: HindIII; Site 2: HindIII; Rice is one of two most popular grains in the world. Half of the world population especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety. The library contains 36,864 clones with an average insert size of 128.5 Kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."

ORIGIN

Query Match 1.6%; Score 29; DB 28; Length 537;  
 Best Local Similarity 100.0%; Pred. No. 0.58;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AAAATAATAATAATTCCAAATTTTTT 56  
 |||||  
 Db 445 AAAATAATAATAATTCCAAATTTTTT 417

RESULT 7  
 LOCUS CG408907/c

DEFINITION CG408907 331 bp DNA linear GSS 03-SEP-2003  
 genomic, genomic survey sequence.

ACCESSION CG408907  
 VERSION CG408907.1 GI:34430272  
 KEYWORDS GSS.  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 331)  
 AUTHORS Kim, C.M., Piao, H.L., Park, S.J., Chon, N.S., Je, B.I., Sun, B., Park, S.H., Park, J.Y., Lee, E.J., Kim, M.J., Lee, J.J., Nam, M.H., Eun, M.Y. and Han, C.D.

TITLE Rapid, large-scale generation of Ds transposon lines and analysis of Ds loci in rice  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Chang-deok Han

Division of Applied Life Science, PMBBRC  
 Gyeongsang National University  
 Gajwa-dong 900, Jinju 660-701, South Korea  
 Tel: +82 55 751 6029  
 Fax: +82 55 759 9363

Email: cdhan@nongae.gsnu.ac.kr  
 Location: chromosome 4 clone OSJNBb0034G17  
 Class: transposon-tagged.

FEATURES  
 source  
 Location/Qualifiers

1..331  
 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="genomic DNA"  
 /cultivar="Dongjin"  
 /db\_xref="taxon:39947"  
 /clone\_lib="Ds insertion lines"

ORIGIN  
 Query Match 1.6%; Score 28; DB 29; Length 331;  
 Best Local Similarity 100.0%; Pred. No. 2.1;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 AATAAGACGAGTGGTCAACAGTACAAG 84  
 |||||  
 Db 220 AATAAGACGAGTGGTCAACAGTACAAG 193

RESULT 8  
 LOCUS AQ331226/c

DEFINITION AQ331226 409 bp DNA linear GSS 16-DEC-1999  
 nbx0049E15r CUGI Rice BAC Library Oryza sativa (japonica cultivar-group) genomic clone nbx0049E15r, genomic survey sequence.

ACCESSION AQ331226  
 VERSION AQ331226.2 GI:6591316  
 KEYWORDS GSS.  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 409)  
 AUTHORS Wing, R.A. and Dean, R.A.  
 TITLE A BAC End Sequencing Framework to Sequence the Rice Genome  
 JOURNAL Unpublished (1998)  
 COMMENT On Dec 15, 1999 this sequence version replaced gi:4123076.

Contact: Wing RA

Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Tel: 864 656 7288

Fax: 864 656 4293  
Email: twing@clemson.edu  
Seq primer: GGAACACGCTATGACCATG  
Class: BAC ends  
High quality sequence stop: 1.

FEATURES  
source  
Location/Qualifiers

1. 409  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="genomic DNA"

/strain="Japonica"  
/cultivar="Nipponbare"

/db\_xref="taxon:39947"  
/clone="nxb0049e15r"

/tissue\_type="Leaf"  
/lab\_host="E. coli DH10B"

/clone\_lib="CUGI Rice BAC Library"  
/notes="Vector: pBeloBAC11; Site 1: HindIII; Site 2:

HindIII; Rice is one of two most popular grains in the world. Half of the world population especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety. The library contains 36,864 clones with an average insert size of 128.5 Kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."

## ORIGIN

Query Match 1.6%; Score 28; DB 28; Length 409;  
Best Local Similarity 100.0%; Pred. No. 1.8;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 ATTTTAAATACAGAGTGTCACAC 76  
|||||  
Db 287 ATTTTAAATACAGAGTGTCACAC 260

## RESULT 9

AQ860090

LOCUS

DEFINITION  
nbe0014121f CUGI Rice BAC Library (EcoRI) Oryza sativa (Japonica cultivar-group) genomic clone nbe0014121f, genomic survey sequence.

ACCESSION  
AQ860090

VERSION  
AQ860090.1 GI:6210547

KEYWORDS  
GSS.

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 452)

Wing, R.A. and Dean, R.A.

A BAC End Sequencing Framework to Sequence the Rice Genome

Unpublished (1998)

Contact: Wing RA

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293  
Email: twing@clemson.edu  
Seq primer: TAATACGACTCATATAGGG  
Class: BAC ends  
High quality sequence start: 31  
High quality sequence stop: 404.

FEATURES  
source  
Location/Qualifiers

1. 452

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="genomic DNA"

/strain="Japonica"

/cultivar="Nipponbare"

/db\_xref="taxon:39947"

/clone="nbe0014121f"

/tissue\_type="Leaf"

/lab\_host="E. coli DH10B"

/clone\_lib="CUGI Rice BAC Library (EcoRI)"

/notes="Vector: pBACIndigo; Site 1: EcoRI; Site 2: EcoRI; Rice is the most important food crop in the world. Half of the world population, especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety using EcoRI as the cloning enzyme. The library contains 55,296 clones with an average insert size of 121 Kb providing approximately 15 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Three high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening and can be requested from the Clemson University BAC/EST Resource Center (www.genome.clemson.edu)."

## ORIGIN

Query Match 1.6%; Score 28; DB 28; Length 452;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 TTTTAAATACAGAGTGTCACACA 77  
|||||  
Db 395 TTTTAAATACAGAGTGTCACACA 422

## RESULT 10

AQ863506/c

LOCUS

DEFINITION

AQ863506 466 bp DNA linear GSS 03-NOV-1999  
nbe0021007f CUGI Rice BAC Library (EcoRI) Oryza sativa (Japonica cultivar-group) genomic clone nbe0021007f, genomic survey sequence.

ACCESSION  
AQ863506

VERSION  
AQ863506.1 GI:6213963

KEYWORDS  
GSS.

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 466)

Wing, R.A. and Dean, R.A.

A BAC End Sequencing Framework to Sequence the Rice Genome

Unpublished (1998)

Contact: Wing RA

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293

Email: rwing@clmson.edu  
 Seq primer: TAATACGACTCACTATAGG  
 Class: BAC ends  
 High quality sequence start: 28  
 High quality sequence stop: 438.  
 Location/Qualifiers  
 1. 466  
 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="genomic DNA"  
 /strain="Japonica"  
 /cultivar="Nipponbare"  
 /db\_xref="taxon:39947"  
 /clone="nbcb0021007f"  
 /tissue\_type="Leaf"  
 /lab\_host="E. coli DH10B"  
 /clone\_lib="CUGI Rice BAC Library (EcoRI)"  
 /note="Vector: pBRACindigo; Site 1: EcoRI; Site 2: EcoRI; Rice is the most important food crop in the world. Half of the world population, especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety using EcoRI as the cloning enzyme. The library contains 55,296 clones with an average insert size of 121 Kb providing approximately 15 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Three high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening and can be requested from the Clemson University BAC/EST Resource Center ([www.genome.clemson.edu](http://www.genome.clemson.edu))."

## FEATURES

source

Seq primer: GGAAACAGCTATGACCATG  
 Class: BAC ends  
 High quality sequence stop: 286.  
 Location/Qualifiers  
 1. 623  
 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="genomic DNA"  
 /strain="Japonica"  
 /cultivar="Nipponbare"  
 /db\_xref="taxon:39947"  
 /clone="nbxb0019P11r"  
 /tissue\_type="Leaf"  
 /lab\_host="E. coli DH10B"  
 /clone\_lib="CUGI Rice BAC Library"  
 /note="Vector: pBeloBAC11; Site 1: HindIII; Site 2: HindIII; Rice is one of two most popular grains in the world. Half of the world population especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety. The library contains 36,864 clones with an average insert size of 128.5 Kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."

## ORIGIN

Query Match 1.6%; Score 28; DB 28; Length 623;  
 Best Local Similarity 100.0%; Pred. No. 1.3;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 ATTTTAAATAAGACGAGTGTCAAAAC 76  
 |||||  
 DB 283 ATTTTAAATAAGACGAGTGTCAAAAC 256

RESULT 12  
 BM420232  
 LOCUS  
 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

BM420232 652 bp mRNA linear EST 28-JAN-2002  
 U004F12 Oryza sativa mature leaf library induced by M.grisea Oryza sativa cDNA clone U004F12, mRNA sequence.  
 BM420232  
 EST.  
 Oryza sativa  
 Oryza sativa

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

1 (bases 1 to 652)  
 Dong, H.T., Li, D.B., Zhuang, X.F., Dai, C.G., Sun, L.X., Pei, Y.X., Wu, H.F., Jiang, Y.X., Yu, F.C., Gao, Q.K. and Lou, Y.C.  
 A Gene Expression Screen in Oryza sativa  
 Unpublished (2001)  
 Contact: Haitao Dong, Debao Li  
 Bioinformatics and Gene Network Research Group  
 Zhejiang University  
 Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.China  
 Tel: 0086-571-86892051  
 Fax: 0086-571-868961525  
 Email: webmaster@estarray.org, URL: <http://www.estarray.org>  
 Seq primer: M13 forward primer.  
 Location/Qualifiers  
 1. 652  
 /organism="Oryza sativa"

/mol\_type="mRNA"  
 /db\_xref="taxon:4530"  
 /clone="U004F12"  
 /tissue\_type="leaf"  
 /dev\_stage="Mature stage"  
 /clone\_lib="Oryza sativa mature leaf library induced by  
 M.grisea"  
 /note="Vector: pSport2"

ORIGIN

Query Match 1.6%; Score 28; DB 12; Length 652;  
 Best Local Similarity 100.0%; Pred. No. 1.3;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 AATAAGACGAGTGTCAAAACAGTACAAG 84  
 ||||||||||||||||||||||||||||||||  
 Db 542 AATPAGACGAGTGTCAAAACAGTACAAG 569

RESULT 13  
 BZ692356  
 LOCUS  
 DEFINITION  
 SP\_Ba0019009.f SP\_Ba Sorghum propinquum genomic clone  
 BZ692356  
 VERSION  
 BZ692356.1 GI:28384160  
 GSS.  
 SOURCE  
 Sorghum propinquum  
 ORGANISM  
 Sorghum propinquum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Sorghum.  
 1 (bases 1 to 694)  
 AUTHORS  
 Wing, R., Yu, Y., Kim, H.R., Collura, K., Pries, G., Currie, J.,  
 Soderlund, C., and Hatfield, J.  
 TITLE  
 Sequencing of Sorghum BAC ends.  
 JOURNAL  
 http://genome.arizona.edu/stc/sorghum  
 COMMENT  
 Unpublished (2003)  
 Contact: Rod Wing  
 Arizona Genomics Institute  
 University of Arizona  
 Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ  
 85721-0088, USA  
 Tel: 520 626 3967  
 Fax: 520 621 9288  
 Email: http://genome.arizona.edu  
 PCR Primers  
 FORWARD: atc agc ggc cgc gat cc  
 BACKWARD: gta aaa cga cgg cca gtg  
 Plate: 0019 row: 0 column: 09  
 Seq primer: atc agc ggc cgc gat cc  
 Class: BAC ends.

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 GSS.  
 SOURCE  
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 ORGANISM  
 Sorghum propinquum  
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 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Sorghum.  
 1 (bases 1 to 694)  
 AUTHORS  
 Wing, R., Yu, Y., Kim, H.R., Collura, K., Pries, G., Currie, J.,  
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 http://genome.arizona.edu/stc/sorghum  
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 85721-0088, USA  
 Tel: 520 626 3967  
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 Email: http://genome.arizona.edu  
 PCR Primers  
 FORWARD: atc agc ggc cgc gat cc  
 BACKWARD: gta aaa cga cgg cca gtg  
 Plate: 0019 row: 0 column: 09  
 Seq primer: atc agc ggc cgc gat cc  
 Class: BAC ends.

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 CC692659  
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 Zea mays  
 ORGANISM  
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 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 783)  
 AUTHORS  
 Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,  
 Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,  
 Citek, R.W., Nunberg, A., Robbins, D., and Lakey, N.  
 Consortium for Maize Genomics  
 Unpublished (2002)  
 Other GSSs: OGTAI20TC  
 Contact: Cathy Whitelaw  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301-838-5843  
 Fax: 301-838-0208  
 Email: whitelaw@tigr.org  
 Seq primer: TR  
 Class: sheared ends.

FEATURES  
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 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 787)  
 AUTHORS  
 Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,  
 Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,  
 Citek, R.W., Nunberg, A., Robbins, D., and Lakey, N.  
 Consortium for Maize Genomics  
 Unpublished (2002)  
 Other GSSs: OGTAI20TH  
 Contact: Cathy Whitelaw  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301-838-5843  
 Fax: 301-838-0208

RESULT 16  
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 VERSION  
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 SOURCE  
 Zea mays  
 ORGANISM  
 Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 787)  
 AUTHORS  
 Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,  
 Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,  
 Citek, R.W., Nunberg, A., Robbins, D., and Lakey, N.  
 Consortium for Maize Genomics  
 Unpublished (2002)  
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 Contact: Cathy Whitelaw  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301-838-5843  
 Fax: 301-838-0208

Email: whitelaw@tigr.org  
Seq primer: Tg  
Class: sheared ends.

FEATURES  
source Location/Qualifiers

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/clone\_lib="ZM\_0.7-1.5\_KB"  
/note="vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb  
methylation filtered genomic DNA library"

ORIGIN

Query Match 1.6%; Score 28; DB 29; Length 787;  
Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Search completed: October 2, 2004, 15:13:13  
Job time : 6892 secs